



SEQUENCE LISTING

<110> Brigham & Women's Hospital

<120> NOVEL COCHLEAR GENE COCH5B2 AND USES THEREOF

<130> 10286/008WO1

<140> PCT/US99/22645

<141> 1999-09-29

<150> US 60/102,343

<151> 1998-09-29

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2534

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (57)...(1706)

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Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu Leu		
5	10	15

ctg ccg ggg ccc gcg ggc agc gag gga gcc gct ccc att gct atc aca	155	
Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile Thr		
20	25	30

tgt ttt acc aga ggc ttg gac atc agg aaa gag aaa gca gat gtc ctc	203	
Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val Leu		
35	40	45

tgc cca ggg ggc tgc cct ctt gag gaa ttc tct gtg tat ggg aac ata	251		
Cys Pro Gly Gly Cys Pro Leu Glu Phe Ser Val Tyr Gly Asn Ile			
50	55	60	65

gta tat gct tct gta tcg agc ata tgt ggg gct gtc cac agg gga	299	
Val Tyr Ala Ser Val Ser Ile Cys Gly Ala Ala Val His Arg Gly		
70	75	80

gta atc agc aac tca ggg gga cct gta cga gtc tat agc cta cct ggt	347	
Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro Gly		
85	90	95

cga gaa aac tat tcc tca gta gat gcc aat ggc atc cag tct caa atg	395	
Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln Met		
100	105	110

ctt tct aga tgg tct gct ttc aca gta act aaa ggc aaa agt agt	443	
Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser Ser		
115	120	125

~~2/12~~ 85

aca cag gag gcc aca gga caa gca gtg tcc aca gca cat cca cca aca		491
Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro Thr		
130 135 140 145		
ggt aaa cga cta aag aaa aca ccc gag aag aaa act ggc aat aaa gat		539
Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys Asp		
150 155 160		
tgt aaa gca gac att gca ttt ctg att gat gga agc ttt aat att ggg		587
Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile Gly		
165 170 175		
cag cgc cga ttt aat tta cag aag aat ttt gtt gga aaa gtg gct cta		635
Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala Leu		
180 185 190		
atg ttg gga att gga aca gaa gga cca cat gtg ggc ctt gtt caa gcc		683
Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln Ala		
195 200 205		
agt gaa cat ccc aaa ata gaa ttt tac ttg aaa aac ttt aca tca gcc		731
Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser Ala		
210 215 220		
aaa gat gtt ttg ttt gcc ata aag gaa gta ggt ttc aga ggg ggt aat		779
Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Asn		
230 235 240		
tcc aat aca gga aaa gcc ttg aag cat act gct cag aaa ttc ttc acg		827
Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe Thr		
245 250 255		
gta gat gct gga gta aga aaa ggg atc ccc aaa gtg gtg gtg gta ttt		875
Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val Phe		
260 265 270		
att gat ggt tgg cct tct gat gac atc gag gaa gca ggc att gtg gcc		923
Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val Ala		
275 280 285		
aga gag ttt ggt gtc aat gta ttt ata gtt tct gtg gcc aag cct atc		971
Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro Ile		
290 295 300		
cct gaa gaa ctg ggg atg gtt cag gat gtc aca ttt gtt gac aag gct		1019
Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys Ala		
310 315 320		
gtc tgt cgg aat aat gcc ttc ttc tct tac cac atg ccc aac tgg ttt		1067
Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp Phe		
325 330 335		
ggc acc aca aaa tac gta aag cct ctg gta cag aag ctg tgc act cat		1115
Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr His		
340 345 350		
gaa caa atg atg tgc agc aag acc tgt tat aac tca gtg aac att gcc		1163
Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile Ala		
355 360 365		
ttt cta att gat ggc tcc agc agt gtt gga gat agc aat ttc cgc ctc		1211
Phe Leu Ile Asp Gly Ser Ser Val Gly Asp Ser Asn Phe Arg Leu		
370 375 380		
atg ctt gaa ttt gtt tcc aac ata gcc aag act ttt gaa atc tcg gac		1259
Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser Asp		
390 395 400		

3/12 86

att ggt gcc aag ata gct gct gta cag ttt act tat gat cag cgc acg Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg Thr 405 410 415	1307
gag ttc agt ttc act gac tat agc acc aaa gag aat gtc cta gct gtc Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala Val 420 425 430	1355
atc aga aac atc cgc tat atg agt ggt gga aca gct act ggt gat gcc Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp Ala 435 440 445	1403
att tcc ttc act gtt aga aat gtg ttt ggc cct ata agg gag agc ccc Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser Pro 450 455 460 465	1451
aac aag aac ttc cta gta att gtc aca gat ggg cag tcc tat gat gat Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp Asp 470 475 480	1499
gtc caa ggc cct gca gct gct gca cat gat gca gga atc act atc ttc Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile Phe 485 490 495	1547
tct gtt ggt gtg gct tgg gca cct ctg gat gac ctg aaa gat atg gct Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met Ala 500 505 510	1595
tct aaa ccg aag gag tct cat gct ttc ttc aca aga gag ttc aca gga Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr Gly 515 520 525	1643
tta gaa cca att gtt tct gat gtc atc aga ggc att tgt aga gat ttc Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp Phe 530 535 540 545	1691
tta gaa tcc cag caa taatggtaac attttgacaa ctgaaaagaaa aagtacaagg Leu Glu Ser Gln Gln 550	1746
ggatccagtg tgtaaattgt attctcataa tactgaaatg ctttagcata ctagaatcg atacaaaact attaagtatg tcaacagcca tttaggc当地 taagcactcc tttaaagccg ctgcctctg gttacaattt acagtgtact ttgttaaaaa cactgctgag gcttcataat catggctctt agaaacttag gaaagaggag ataatgtgga ttaaaacctt aagagttcta accatgccta ctaaatgtac agatatgca attccatacg tcaataaaag aatctgatac tttagacaaa agcaacattc gttctctaac cattctgtat tgattatata agcaaaatga aaagagaaaac tttaaatgaaac acagctttt aacatgggtc aggtacacat attttgaccc aagtggatat ttctttttt ccaatcaata atagctgatcattactgtag actataaaaat ctggatataag aaggagacc ttttatcaaact tgcttttgc tggttttc ttatatttc atgactaaaa atatcacact gaataagaga gcaggatgc caggtatccc tctatttc tccttaattt tatatgtata tagatatatt tggcttatat tcttaagtcc ctaagtactt aaaagtttaag ttggtaaagt atttactgac tgcttataaa cattaaaga caaagacatt tcaaataact gcagaaaaaaa tatttgttgc tgaatattt acaataaaa ctgctgt gttatttgt	1806 1866 1926 1986 2046 2106 2166 2226 2286 2346 2406 2466 2526 2534

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<212> PRT
<213> *Homo sapiens*

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~~4/12~~ 87

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
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Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
50 55 60
Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
65 70 75 80
Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
85 90 95
Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
100 105 110
Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
115 120 125
Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
130 135 140
Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
145 150 155 160
Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
165 170 175
Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
180 185 190
Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
195 200 205
Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
210 215 220
Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly
225 230 235 240
Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
245 250 255
Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val
260 265 270
Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
275 280 285
Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
290 295 300
Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
305 310 315 320
Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
325 330 335
Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
340 345 350
His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
355 360 365
Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
370 375 380
Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
385 390 395 400
Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
405 410 415
Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
420 425 430
Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
435 440 445
Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
450 455 460
Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
465 470 475 480
Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
485 490 495
Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
500 505 510
Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
515 520 525
Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
530 535 540
Phe Leu Glu Ser Gln Gln
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5/12 88

<210> 3

<211> 1650

<212> DNA

<213> Homo sapiens

<400> 3

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ttcacagtaa	ctaaaaggca	aagttagtaca	caggaggcca	caggacaagc	agtgtccaca	420
gcacatccac	caacaggtaa	acgactaaag	aaaacacccc	agaagaaaac	tggcaataaa	480
gattgttaaag	cagacattgc	atttctgtt	gatggaaagt	ttaatattgg	gcagcggcga	540
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aactttatcat	cagccaaaga	tgttttgtt	gccataaagg	aagttagttt	cagaggggt	720
aattccaata	cagggaaaagc	tttgaagcat	actgctcaga	aattcttcac	ggttagatgt	780
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ataagggaga	gccccaaacaa	gaacttctta	gtaattgtca	cagatggca	gtcctatgtat	1440
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gtggcttggg	cacctctgga	tgacctgaaa	gatatggctt	ctaaaccgaa	ggagtctcat	1560
gctttcttca	caagagagtt	cacaggatta	gaaccaattt	tttctgtatgt	catcagaggc	1620
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<211> 145

<212> PRT

<213> Homo sapiens

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									20				25		30
Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln	Ala	Ser	Glu	His
									35				40		45
Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser	Ala	Lys	Asp	Val
									50				55		60
Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly	Asn	Ser	Asn	Thr
									65				70		75
Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe	Thr	Val	Asp	Ala
									85				90		95
Gly	Val	Arg	Lys	Gly	Ile	Pro	Lys	Val	Val	Val	Val	Phe	Ile	Asp	Gly
									100				105		110
Trp	Pro	Ser	Asp	Asp	Ile	Glu	Glu	Ala	Gly	Ile	Val	Ala	Arg	Glu	Phe
									115				120		125
Gly	Val	Asn	Val	Phe	Ile	Val	Ser	Val	Ala	Lys	Pro	Ile	Pro	Glu	Glu
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Leu															
145															

<210> 5

<211> 149

<212> PRT

<213> Homo sapiens

6122 89

<400> 5

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Glu Ile Ser Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr
35 40 45
Asp Gln Arg Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn
50 55 60
val Leu Ala Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala
65 70 75 80
Thr Gly Asp Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile
85 90 95
Arg Glu Ser Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln
100 105 110
Ser Tyr Asp Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly
115 120 125
Ile Thr Ile Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu
130 135 140
Lys Asp Met Ala Ser
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<210> 6

<211> 2455

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (69)...(1725)

<400> 6

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Met Pro Ser Ser Arg Ile Pro Ala Leu Cys Leu Gly Ala Trp
1 5 10

ctg ctg ctg ctg ctg ccc cgg ttc gcg cgcc gcc gag gga gcg gtt 158
Leu Leu Leu Leu Leu Pro Arg Phe Ala Arg Ala Glu Gly Ala Val
15 20 25 30

ccc att cct gtc acc tgc ttt acc aga ggc ctg gat atc cga aaa gag 206
Pro Ile Pro Val Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu
35 40 45

aaa gca gat gtt ctc tgc cca gga ggc tgc tct ctt gag gaa ttc tct 254
Lys Ala Asp Val Leu Cys Pro Gly Gly Cys Ser Leu Glu Glu Phe Ser
50 55 60

gtg ttt ggg aac ata gtg tat gcg tca gtg tcc agc atc tgc ggc gct 302
Val Phe Gly Asn Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala
65 70 75

gct gtc cat agg gga gtg att ggc acc tca ggg gga cct gtg cgt gtc 350
Ala Val His Arg Gly Val Ile Gly Thr Ser Gly Gly Pro Val Arg Val
80 85 90

tac agc ctt cct ggt cga gag aac tac tcc tgc gta gat gcc aac ggc 398
Tyr Ser Leu Pro Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly
95 100 105 110

atc cag tct cag atg ctt tcc cga tgg tcc gcg tcc ttc gct gtg acc 446
Ile Gln Ser Gln Met Leu Ser Arg Trp Ser Ala Ser Phe Ala Val Thr
115 120 125

~~7412~~ 90

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gcc cac cca cct tca ggt aaa aga cta aag aag aca cca gag aag aag Ala His Pro Pro Ser Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys 145 150 155	542
act ggc aac aaa gac tgt aag gca gac att gca ttt ctc att gat gga Thr Gly Asn Lys Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly 160 165 170	590
agc ttc aat att ggg cag cgc cga ttt aat ttg cag aag aat ttt gtt Ser Phe Asn Ile Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val 175 180 185 190	638
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aac ttt act tca gcc aaa gat gtc ttg ttt gcc ata aaa gaa gta ggt Asn Phe Thr Ser Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly 225 230 235	782
ttc cga ggg ggt aac tcc aac aca gga aaa gcc ttg aag cac act gct Phe Arg Gly Gly Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala 240 245 250	830
cag aaa ttc ttt aca gca gac act ggt gtg aga aaa gga ata cca aaa Gln Lys Phe Phe Thr Ala Asp Thr Gly Val Arg Lys Gly Ile Pro Lys 255 260 265 270	878
gtg gtg gta gtg ttt att gat ggt tgg ccc tct gat gac att gag gaa Val Val Val Val Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu 275 280 285	926
gca ggc att gtg gcc aga gag ttt ggt gtc aat gta ttt ata gtt tct Ala Gly Ile Val Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser 290 295 300	974
gtg gcc aag ccc att cct gaa gaa ctg ggg atg gtt caa gat gtt gca Val Ala Lys Pro Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Ala 305 310 315	1022
ttt gtt gac aag gct gtg tgt cgg aat aat ggc ttc ttc tct tat cac Phe Val Asp Lys Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His 320 325 330	1070
atg ccc aac tgg ttt ggc act aca aaa tat gtg aag cct ctg gtg cag Met Pro Asn Trp Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln 335 340 345 350	1118
aag ctc tgt acg cac gaa cag atg atg tgc agc aaa acc tgc tac aac Lys Leu Cys Thr His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn 355 360 365	1166
tca gtg aac att gcc ttt ctg att gac ggc tcc agc agt gtt gga gat Ser Val Asn Ile Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp 370 375 380	1214
agc aat ttc cgc ctc atg cta gaa ttt gtt tct aac ata gcg aag aca Ser Asn Phe Arg Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr 385 390 395	1262

~~8/12~~ 91

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Phe Glu Ile Ser Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr	
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tat gac cag cgc acc gag ttc agt ttc act gac tat aat acc aaa gag	1358
Tyr Asp Gln Arg Thr Glu Phe Ser Phe Thr Asp Tyr Asn Thr Lys Glu	
415 420 425 430	
aac gtc cta gct gtc cta gcg aac atc cgc tac atg agt ggt ggc aca	1406
Asn Val Leu Ala Val Leu Ala Asn Ile Arg Tyr Met Ser Gly Gly Thr	
435 440 445	
gct act ggt gat gcc atc gcc ttt act gtt aga aat gta ttt ggt ccc	1454
Ala Thr Gly Asp Ala Ile Ala Phe Thr Val Arg Asn Val Phe Gly Pro	
450 455 460	
ata agg gac agc ccc aac aaa aac ttc ctg gtt att gtc aca gat ggg	1502
Ile Arg Asp Ser Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly	
465 470 475	
cag tcc tat gat gat gtc cga ggc cct gct gca gct gcc cat gat gca	1550
Gln Ser Tyr Asp Asp Val Arg Gly Pro Ala Ala Ala His Asp Ala	
480 485 490	
ggg atc acc atc ttc tct gtt ggt gtg gct tgg gca ccg ctg gat gac	1598
Gly Ile Thr Ile Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp	
495 500 505 510	
ctg aga gat atg gcc tct aaa ccc aaa gag tca cac gct ttc ttt acc	1646
Leu Arg Asp Met Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr	
515 520 525	
aga gag ttc aca ggg tta gaa cca att gtc tct gac gtc atc aga ggc	1694
Arg Glu Phe Thr Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly	
530 535 540	
att tgt aga gac ttc tta gaa tcc cag caa t aaccgatact ctgacaactc	1745
Ile Cys Arg Asp Phe Leu Glu Ser Gln Gln	
545 550	
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gatgctcaca atttagattt gcccggactt gataatcagg cccttagaaaa ctcaggaaag	1925
aagagttgtc atggatataac attgggagtt caaatatgca ttcaagtgg taggttaagct	1985
acacagctca ataaaagaac ctggcgctt cacacaaagc actgtttccct cttaatcac	2045
tctgcattga ccatgcaagg aaaacagaac agctttaaa cacagatcaa gtatacatat	2105
tttgaccat gtggatgttt tcttaaaacc agccaagaac agacagctgt tattatgtgc	2165
actagccata actacacatt atatggaatc atatatcaag cttttttgt agtgtgtttt	2225
cataacctga tggctgaaat accacactga gtaaaggtag gattgcctgg tattttctta	2285
tttatatcct taatttttag tgtatagaca ggcatgtact ccgaggacta agaaaatgtt	2345
taagcagata acctttttt ttggaaaaaaa aagatgtgtc aagtattgtt accgaaaaaaa	2405
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<211> 552	
<212> PRT	
<213> Mus musculus	
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Met Pro Ser Ser Arg Ile Pro Ala Leu Cys Leu Gly Ala Trp Leu Leu	
1 5 10 15	
Leu Leu Leu Leu Pro Arg Phe Ala Arg Ala Glu Gly Ala Val Pro Ile	
20 25 30	
Pro Val Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala	
35 40 45	

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Asp Val Leu Cys Pro Gly Gly Cys Ser Leu Glu Glu Phe Ser Val Phe
50 55 60
Gly Asn Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val
65 70 75 80
His Arg Gly Val Ile Gly Thr Ser Gly Gly Pro Val Arg Val Tyr Ser
85 90 95
Leu Pro Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln
100 105 110
Ser Gln Met Leu Ser Arg Trp Ser Ala Ser Phe Ala Val Thr Lys Gly
115 120 125
Lys Ser Ser Thr Gln Glu Ala Thr Gly Arg Ala Val Ser Thr Ala His
130 135 140
Pro Pro Ser Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly
145 150 155 160
Asn Lys Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe
165 170 175
Asn Ile Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys
180 185 190
Val Ala Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu
195 200 205
Val Gln Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe
210 215 220
Thr Ser Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg
225 230 235 240
Gly Gly Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys
245 250 255
Phe Phe Thr Ala Asp Thr Gly Val Arg Lys Gly Ile Pro Lys Val Val
260 265 270
Val Val Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly
275 280 285
Ile Val Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala
290 295 300
Lys Pro Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Ala Phe Val
305 310 315 320
Asp Lys Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro
325 330 335
Asn Trp Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu
340 345 350
Cys Thr His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val
355 360 365
Asn Ile Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn
370 375 380
Phe Arg Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu
385 390 395 400
Ile Ser Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp
405 410 415
Gln Arg Thr Glu Phe Ser Phe Thr Asp Tyr Asn Thr Lys Glu Asn Val
420 425 430
Leu Ala Val Leu Ala Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr
435 440 445
Gly Asp Ala Ile Ala Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg
450 455 460
Asp Ser Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser
465 470 475 480
Tyr Asp Asp Val Arg Gly Pro Ala Ala Ala His Asp Ala Gly Ile
485 490 495
Thr Ile Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Arg
500 505 510
Asp Met Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu
515 520 525
Phe Thr Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys
530 535 540
Arg Asp Phe Leu Glu Ser Gln Gln
545 550

<210> 8
<211> 149

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<212> PRT

<213> Homo sapiens

<400> 8

Asp Leu Val Phe Leu Val Asp Gly Ser Trp Ser Val Gly Arg Asn Asn
1 5 10 15
Phe Lys Tyr Ile Leu Asp Phe Ile Ala Ala Leu Val Ser Ala Phe Asp
20 25 30
Ile Gly Glu Glu Lys Thr Arg Val Gly Val Val Gln Tyr Ser Ser Asp
35 40 45
Thr Arg Thr Glu Phe Asn Leu Asn Gln Tyr Tyr Gln Arg Asp Glu Leu
50 55 60
Leu Ala Ala Ile Lys Lys Ile Pro Tyr Lys Gly Gly Asn Thr Met Thr
65 70 75 80
Asp Ala Ile Asp Tyr Leu Val Lys Asn Thr Phe Thr Glu Ser Ala Gly
85 90 95
Ala Arg Val Gly Phe Pro Lys Val Ala Ile Ile Thr Asp Gly Lys
100 105 110
Ser Gln Asp Glu Val Glu Ile Pro Ala Arg Glu Leu Arg Asn Val Gly
115 120 125
Val Glu Val Phe Ser Leu Gly Ile Lys Ala Ala Asp Ala Lys Glu Leu
130 135 140
Lys Gln Ile Ala Ser
145

<210> 9

<211> 145

<212> PRT

<213> Homo sapiens

<400> 9

Asp Leu Val Phe Leu Ile Asp Gly Ser Lys Ser Val Arg Pro Glu Asn
1 5 10 15
Phe Glu Leu Val Lys Lys Phe Glu Ser Gln Ile Val Asp Thr Leu Asp
20 25 30
Val Ser Asp Lys Leu Ala Gln Val Gly Leu Val Gln Tyr Ser Ser Ser
35 40 45
Val Arg Gln Glu Phe Pro Leu Gly Arg Phe His Thr Lys Lys Asp Ile
50 55 60
Lys Ala Ala Val Arg Asn Met Ser Tyr Met Glu Lys Gly Thr Met Thr
65 70 75 80
Gly Ala Ala Leu Lys Tyr Leu Ile Asp Asn Ser Phe Thr Val Ser Ser
85 90 95
Gly Ala Arg Pro Gly Ala Gln Lys Val Gly Ile Val Phe Thr Asp Gly
100 105 110
Arg Ser Gln Asp Tyr Ile Asn Asp Ala Ala Lys Lys Ala Lys Asp Leu
115 120 125
Gly Phe Lys Met Phe Ala Val Gly Val Gly Asn Ala Val Glu Asp Glu
130 135 140
Leu
145

<210> 10

<211> 137

<212> PRT

<213> Homo sapiens

<400> 10

Asp Val Ile Leu Leu Leu Asp Gly Ser Ser Ser Phe Pro Ala Ser Tyr
1 5 10 15
Phe Asp Glu Met Lys Ser Phe Ala Lys Ala Phe Ile Ser Lys Ala Asn
20 25 30
Ile Gly Pro Arg Leu Thr Gln Val Ser Val Leu Gln Tyr Gly Ser Ile
35 40 45
Thr Thr Ile Asp Val Pro Trp Asn Val Val Pro Glu Lys Ala His Leu
50 55 60

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Leu Ser Leu Val Asp Val Asn Gln Arg Glu Gly Gly Pro Ser Gln Ile
65 70 75 80
Gly Asp Ala Leu Gly Phe Ala Val Arg Tyr Leu Thr Ser Glu Met His
85 90 95
Gly Ala Arg Pro Gly Ala Ser Lys Ala Val Val Ile Leu Val Thr Asp
100 105 110
Val Ser Val Asp Ser Val Asp Ala Ala Ala Asp Ala Ala Arg Ser Asn
115 120 125
Arg Val Thr Val Phe Pro Ile Gly Ile
130 135

<210> 11
<211> 105
<212> PRT
<213> Homo sapiens

<400> 11
Ile Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp
1 5 10 15
Val Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly
20 25 30
Asn Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His
35 40 45
Arg Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu
50 55 60
Pro Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser
65 70 75 80
Gln Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys
85 90 95
Ser Ser Thr Gln Glu Ala Thr Gly Gln
100 105

<210> 12
<211> 20
<212> DNA
<213> Unknown

<220>
<223> probe

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gattgtaaag cagacattgc 20

<210> 13
<211> 17
<212> DNA
<213> Unknown

<220>
<223> probe

<400> 13
acctacttcc ttatggc 17

<210> 14
<211> 20
<212> DNA
<213> Unknown

<220>
<223> probe

<400> 14
ggcgcgttc atgtatgtgt 20

<210> 15
<211> 20

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<212> DNA
<213> Unknown

<220>
<223> probe

<400> 15
gctatggaat ttgcataatct 20

<210> 16
<211> 20
<212> DNA
<213> Unknown

<220>
<223> primer

<400> 16
catcagaggc agcatttgta 20

<210> 17
<211> 18
<212> DNA
<213> Unknown

<220>
<223> primer

<400> 17
ttgttaaccag aaggcagc 18

<210> 18
<211> 14
<212> DNA
<213> Unknown

<220>
<223> probe

<400> 18
aacatagtat atgc 14

<210> 19
<211> 14
<212> DNA
<213> Unknown

<220>
<223> probe

<400> 19
ttcttagacgg tctg 14